

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 13, 2006, 18:44:16 ; Search time 187 Seconds  
 (without alignments)  
 1743.417 Million cell updates/sec

Title: US-10-725-189-2  
 Perfect score: 3911  
 Sequence: 1 MEEGFRDRAAFIRGAKDIAK.....LALGSSLALKLPETRGQVLQ 742

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

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 1: geneseqp1980s:\*  
 2: geneseqp1990s:\*  
 3: geneseqp2000s:\*  
 4: geneseqp2001s:\*  
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 6: geneseqp2003as:\*  
 7: geneseqp2003bs:\*  
 8: geneseqp2004s:\*  
 9: geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		Length	DB	ID	Description
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1	3911	100.0		742	7	ADE56938	Ade56938 Human Pro
2	3911	100.0		742	8	ADO77821	Ado77821 Human syn
3	3911	100.0		742	8	ADP44582	Adp44582 Human syn
4	3911	100.0		742	8	ABM80187	Abm80187 Tumour-as
5	3906	99.9		742	7	ADJ70526	Adj70526 Human hea
6	3901	99.7		742	3	AAY94977	Aay94977 Human sec
7	3868	98.9		742	7	ADE56936	Ade56936 Rat Prote
8	3868	98.9		742	8	ADO77829	Ado77829 Rat synap

9	3868	98.9	742	8	ADP44590	Adp44590	Norway ra
10	2464.5	63.0	727	6	ABP98503	Abp98503	Rat synap
11	2464.5	63.0	727	7	ADB85198	Adb85198	Rat synap
12	2464.5	63.0	727	7	ADD46636	Add46636	Rat Prote
13	2464.5	63.0	727	8	ADO77833	Ado77833	Rat synap
14	2464.5	63.0	727	8	ADP44594	Adp44594	Norway ra
15	2447.5	62.6	727	8	ADO77825	Ado77825	Human syn
16	2447.5	62.6	727	8	ADP44586	Adp44586	Human syn
17	2439.5	62.4	727	6	AAO26569	Aao26569	Human tra
18	2337	59.8	683	8	ADO77831	Ado77831	Rat synap
19	2337	59.8	683	8	ADP44592	Adp44592	Norway ra
20	2337	59.8	684	7	ADE56999	Ade56999	Rat Prote
21	2325.5	59.5	683	8	ADO77823	Ado77823	Human syn
22	2325.5	59.5	683	8	ADP44584	Adp44584	Human syn
23	1337	34.2	262	4	AAU87674	Aau87674	Novel cen
24	1337	34.2	262	4	ADM20144	Adm20144	Protein e
25	1337	34.2	262	4	ADM19904	Adm19904	Protein e
26	1337	34.2	262	8	ADI54989	Adi54989	Novel hum
27	1337	34.2	265	4	AAU87398	Aau87398	Novel cen
28	1337	34.2	265	8	ADI54713	Adi54713	Novel hum
29	719	18.4	147	5	ABB90065	Abb90065	Human pol
30	691.5	17.7	709	4	ABB59685	Abb59685	Drosophil
31	660	16.9	773	5	AAU96925	Aau96925	Flea syna
32	488.5	12.5	454	8	ADS45030	Ads45030	Bacterial
33	485	12.4	422	8	ADN25838	Adn25838	Bacterial
34	464.5	11.9	438	8	ADS26123	Ads26123	Bacterial
35	464.5	11.9	438	8	ADS25405	Ads25405	Bacterial
36	464.5	11.9	438	8	ADS25643	Ads25643	Bacterial
37	464.5	11.9	438	8	ADS22544	Ads22544	Bacterial
38	453.5	11.6	588	7	ABM88010	Abm88010	Rice abio
39	425	10.9	398	8	ADN17651	Adn17651	Bacterial
40	425	10.9	529	8	ADN23155	Adn23155	Bacterial
41	425	10.9	529	8	ADN23156	Adn23156	Bacterial
42	422	10.8	508	8	ADY07766	Ady07766	Plant ful
43	421	10.8	548	8	ADO77835	Ado77835	Rat synap
44	421	10.8	548	8	ADP44596	Adp44596	Norway ra
45	421	10.8	548	9	ADX26400	Adx26400	Novel cel

# ALIGNMENTS

## RESULT 1

ADE56938

ID ADE56938 standard; protein; 742 AA.

XX

AC ADE56938;

XX

DT 29-JAN-2004 (first entry)

XX

DE Human Protein NP\_055664, SEQ ID NO 2793.

XX

KW Human; pain; neuronal tissue; gene therapy;

KW spinal segmental nerve injury; chronic constriction injury; CCI;

KW spared nerve injury; SNI; Chung.

XX

OS Homo sapiens.

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OM protein - protein search, using sw model

Run on: February 13, 2006, 18:51:52 ; Search time 48 Seconds  
(without alignments)  
1278.028 Million cell updates/sec

Title: US-10-725-189-2  
Perfect score: 3911  
Sequence: 1 MEEGFRDRAAFIRGAKDIAK.....LALGSSLALKLPETRGQVLQ 742

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	538	13.8	455	2	US-09-270-767-46061	Sequence 46061, A
2	409	10.5	439	2	US-09-602-787A-514	Sequence 514, App
3	404	10.3	456	2	US-09-328-352-5446	Sequence 5446, Ap
4	403	10.3	506	2	US-09-252-991A-17560	Sequence 17560, A
5	379	9.7	420	2	US-09-543-681A-6289	Sequence 6289, Ap
6	360.5	9.2	475	2	US-09-328-352-5706	Sequence 5706, Ap
7	310	7.9	465	2	US-09-328-352-7326	Sequence 7326, Ap
8	296.5	7.6	463	2	US-09-489-039A-10827	Sequence 10827, A
9	287.5	7.4	399	2	US-09-602-787A-416	Sequence 416, App
10	276	7.1	470	2	US-09-328-352-6673	Sequence 6673, Ap
11	271.5	6.9	490	2	US-09-252-991A-27210	Sequence 27210, A

12	270	6.9	610	2	US-09-949-016-7929	Sequence 7929, Ap
13	264	6.8	556	2	US-08-501-572-1	Sequence 1, Appli
14	264	6.8	556	2	US-09-040-444-1	Sequence 1, Appli
15	263	6.7	449	2	US-09-328-352-4726	Sequence 4726, Ap
16	262	6.7	502	2	US-09-489-039A-13185	Sequence 13185, A
17	262	6.7	585	2	US-09-248-796A-20176	Sequence 20176, A
18	260	6.6	553	2	US-08-501-572-2	Sequence 2, Appli
19	260	6.6	553	2	US-09-040-444-2	Sequence 2, Appli
20	258	6.6	557	2	US-10-327-189-4	Sequence 4, Appli
21	258	6.6	557	2	US-09-521-195B-3	Sequence 3, Appli
22	258	6.6	557	2	US-09-798-743-1	Sequence 1, Appli
23	258	6.6	557	2	US-09-949-016-6309	Sequence 6309, Ap
24	257.5	6.6	555	2	US-08-501-572-3	Sequence 3, Appli
25	257.5	6.6	555	2	US-09-040-444-3	Sequence 3, Appli
26	254.5	6.5	451	2	US-09-328-352-7659	Sequence 7659, Ap
27	252	6.4	554	2	US-09-949-016-10978	Sequence 10978, A
28	250	6.4	460	2	US-09-489-039A-10519	Sequence 10519, A
29	244	6.2	447	2	US-09-252-991A-20563	Sequence 20563, A
30	242.5	6.2	418	2	US-09-328-352-6461	Sequence 6461, Ap
31	241	6.2	609	2	US-09-949-016-10979	Sequence 10979, A
32	238.5	6.1	529	2	US-09-291-922-28	Sequence 28, Appl
33	237.5	6.1	521	2	US-09-489-039A-9549	Sequence 9549, Ap
34	237.5	6.1	550	2	US-09-330-245A-2	Sequence 2, Appli
35	237.5	6.1	550	2	US-09-614-891-7	Sequence 7, Appli
36	236.5	6.0	444	2	US-09-328-352-6744	Sequence 6744, Ap
37	236	6.0	462	2	US-09-328-352-6888	Sequence 6888, Ap
38	235.5	6.0	446	2	US-09-543-681A-6579	Sequence 6579, Ap
39	235	6.0	513	2	US-09-291-922-20	Sequence 20, Appl
40	234.5	6.0	446	2	US-09-602-787A-602	Sequence 602, App
41	232.5	5.9	538	2	US-09-614-891-9	Sequence 9, Appli
42	232.5	5.9	546	2	US-09-614-891-8	Sequence 8, Appli
43	231.5	5.9	488	2	US-10-162-012-46	Sequence 46, Appl
44	231.5	5.9	547	2	US-09-949-016-7043	Sequence 7043, Ap
45	228.5	5.8	556	2	US-09-949-016-7027	Sequence 7027, Ap

#### ALIGNMENTS

##### RESULT 1

US-09-270-767-46061

; Sequence 46061, Application US/09270767

; Patent No. 6703491

; GENERAL INFORMATION:

; APPLICANT: Homburger et al.

; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*

; FILE REFERENCE: File Reference: 7326-094

; CURRENT APPLICATION NUMBER: US/09/270,767

; CURRENT FILING DATE: 1999-03-17

; NUMBER OF SEQ ID NOS: 62517

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 46061

; LENGTH: 455

; TYPE: PRT

; ORGANISM: *Drosophila melanogaster*

US-09-270-767-46061

OM protein - protein search, using sw model

Run on: February 13, 2006, 18:52:42 ; Search time 171 Seconds  
 (without alignments)  
 1813.037 Million cell updates/sec

Title: US-10-725-189-2  
 Perfect score: 3911  
 Sequence: 1 MEEGFRDRAAFIRGAKDIAK.....LALGSSLALKLPETRGQVLQ 742

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

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 3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*  
 4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
 5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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		Match	Length			
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2	3911	100.0	742	4	US-10-725-189-2	Sequence 2, Appli
3	3906	99.9	742	4	US-10-408-765A-2332	Sequence 2332, Ap
4	3901	99.7	742	3	US-09-374-046A-160	Sequence 160, App
5	3901	99.7	742	4	US-10-616-263-160	Sequence 160, App
6	3868	98.9	742	4	US-10-308-163-10	Sequence 10, Appl
7	3868	98.9	742	4	US-10-725-189-10	Sequence 10, Appl
8	2464.5	63.0	727	3	US-09-822-246-4	Sequence 4, Appli
9	2464.5	63.0	727	4	US-10-170-528-4	Sequence 4, Appli
10	2464.5	63.0	727	4	US-10-205-194-79	Sequence 79, Appl
11	2464.5	63.0	727	4	US-10-308-163-14	Sequence 14, Appl

12	2464.5	63.0	727	4	US-10-725-189-14	Sequence 14, Appl
13	2464.5	63.0	727	5	US-10-469-028-4	Sequence 4, Appli
14	2447.5	62.6	727	4	US-10-308-163-6	Sequence 6, Appli
15	2447.5	62.6	727	4	US-10-725-189-6	Sequence 6, Appli
16	2440	62.4	724	5	US-10-732-923-23894	Sequence 23894, A
17	2439.5	62.4	727	3	US-09-822-246-2	Sequence 2, Appli
18	2439.5	62.4	727	5	US-10-469-028-2	Sequence 2, Appli
19	2337	59.8	683	4	US-10-308-163-12	Sequence 12, Appl
20	2337	59.8	683	4	US-10-725-189-12	Sequence 12, Appl
21	2325.5	59.5	683	4	US-10-308-163-4	Sequence 4, Appli
22	2325.5	59.5	683	4	US-10-725-189-4	Sequence 4, Appli
23	1337	34.2	262	3	US-09-764-875-1192	Sequence 1192, Ap
24	1337	34.2	265	3	US-09-764-875-916	Sequence 916, App
25	719	18.4	147	4	US-10-264-237-2441	Sequence 2441, Ap
26	691.5	17.7	709	6	US-11-097-143-5847	Sequence 5847, Ap
27	660	16.9	773	5	US-10-399-215-9	Sequence 9, Appli
28	488.5	12.5	454	4	US-10-369-493-23460	Sequence 23460, A
29	485	12.4	422	4	US-10-369-493-8491	Sequence 8491, Ap
30	466.5	11.9	588	4	US-10-437-963-159182	Sequence 159182,
31	464.5	11.9	438	4	US-10-369-493-11577	Sequence 11577, A
32	464.5	11.9	438	4	US-10-369-493-14438	Sequence 14438, A
33	464.5	11.9	438	4	US-10-369-493-14676	Sequence 14676, A
34	464.5	11.9	438	4	US-10-369-493-15156	Sequence 15156, A
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36	425	10.9	529	4	US-10-369-493-5808	Sequence 5808, Ap
37	425	10.9	529	4	US-10-369-493-5809	Sequence 5809, Ap
38	422	10.8	508	4	US-10-425-114-63581	Sequence 63581, A
39	421	10.8	548	4	US-10-308-163-16	Sequence 16, Appl
40	421	10.8	548	4	US-10-725-189-16	Sequence 16, Appl
41	414.5	10.6	492	4	US-10-425-115-211942	Sequence 211942,
42	410	10.5	530	3	US-09-991-936-1902	Sequence 1902, Ap
43	410	10.5	530	5	US-10-399-215-3	Sequence 3, Appli
44	410	10.5	530	5	US-10-978-245-1902	Sequence 1902, Ap
45	409	10.5	439	4	US-10-627-476-514	Sequence 514, App

#### ALIGNMENTS

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RESULT 1
US-10-308-163-2
; Sequence 2, Application US/10308163
; Publication No. US20040106147A1
; GENERAL INFORMATION:
; APPLICANT: UCB, S.A.
; APPLICANT: LYNCH, Berkley
; APPLICANT: NOCKA, Karl
; APPLICANT: FUKS, Bruno
; TITLE OF INVENTION: Levetiracetam Binding Site
; FILE REFERENCE: 53529-5007
; CURRENT APPLICATION NUMBER: US/10/308,163
; CURRENT FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 742
; TYPE: PRT

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OM protein - protein search, using sw model

Run on: February 13, 2006, 18:53:32 ; Search time 17 Seconds  
 (without alignments)  
 572.760 Million cell updates/sec

Title: US-10-725-189-2  
 Perfect score: 3911  
 Sequence: 1 MEEGFRDRAAFIRGAKDIAK.....LALGSSLALKLPETRGQVLQ 742

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 97014 seqs, 13122538 residues

Total number of hits satisfying chosen parameters: 97014

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	238.5	6.1	529	7	US-11-210-316-28	Sequence 28, Appl
2	237.5	6.1	550	6	US-10-055-877-274	Sequence 274, App
3	237.5	6.1	550	6	US-10-055-877-275	Sequence 275, App
4	237.5	6.1	563	6	US-10-055-877-273	Sequence 273, App
5	235	6.0	513	7	US-11-210-316-20	Sequence 20, Appl
6	234.5	6.0	446	7	US-11-082-389-316	Sequence 316, App
7	231.5	5.9	488	6	US-10-055-877-231	Sequence 231, App
8	230	5.9	218	7	US-11-082-389-318	Sequence 318, App
9	227.5	5.8	539	7	US-11-210-316-26	Sequence 26, Appl

10	224.5	5.7	551	6	US-10-055-877-276	Sequence 276, App
11	224.5	5.7	551	6	US-10-055-877-277	Sequence 277, App
12	223	5.7	510	7	US-11-210-316-22	Sequence 22, Appl
13	222	5.7	550	7	US-11-043-889-5	Sequence 5, Appli
14	216	5.5	523	7	US-11-210-316-24	Sequence 24, Appl
15	215	5.5	549	7	US-11-210-316-30	Sequence 30, Appl
16	211.5	5.4	538	6	US-10-793-626-3134	Sequence 3134, Ap
17	204	5.2	329	6	US-10-793-626-1942	Sequence 1942, Ap
18	201.5	5.2	432	7	US-11-113-424-186	Sequence 186, App
19	201.5	5.2	737	7	US-11-210-316-8	Sequence 8, Appli
20	194.5	5.0	477	6	US-10-479-873-9	Sequence 9, Appli
21	188.5	4.8	477	6	US-10-479-873-10	Sequence 10, Appl
22	187.5	4.8	556	6	US-10-055-877-81	Sequence 81, Appl
23	187	4.8	729	7	US-11-210-316-29	Sequence 29, Appl
24	184	4.7	573	6	US-10-055-877-79	Sequence 79, Appl
25	181.5	4.6	705	7	US-11-124-367A-353	Sequence 353, App
26	166	4.2	524	7	US-11-113-424-64	Sequence 64, Appl
27	165.5	4.2	747	7	US-11-210-316-2	Sequence 2, Appli
28	160.5	4.1	359	6	US-10-055-877-272	Sequence 272, App
29	160	4.1	522	7	US-11-054-281-124	Sequence 124, App
30	160	4.1	522	7	US-11-054-281-125	Sequence 125, App
31	158	4.0	523	7	US-11-054-281-122	Sequence 122, App
32	153.5	3.9	483	7	US-11-113-424-24	Sequence 24, Appl
33	153	3.9	523	7	US-11-054-281-123	Sequence 123, App
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36	150	3.8	347	6	US-10-055-877-270	Sequence 270, App
37	150	3.8	347	6	US-10-055-877-271	Sequence 271, App
38	146	3.7	400	6	US-10-793-626-3116	Sequence 3116, Ap
39	146	3.7	499	6	US-10-821-234-1106	Sequence 1106, Ap
40	144.5	3.7	295	6	US-10-793-626-2998	Sequence 2998, Ap
41	144	3.7	480	7	US-11-080-991-76	Sequence 76, Appl
42	143.5	3.7	522	7	US-11-010-239-52	Sequence 52, Appl
43	143	3.7	518	6	US-10-821-234-1165	Sequence 1165, Ap
44	139.5	3.6	206	7	US-11-082-389-234	Sequence 234, App
45	139.5	3.6	225	7	US-11-082-389-232	Sequence 232, App

#### ALIGNMENTS

##### RESULT 1

US-11-210-316-28

; Sequence 28, Application US/11210316

; Publication No. US20050282278A1

; GENERAL INFORMATION:

; APPLICANT: Allen, Stephen M.

; APPLICANT: Hitz, William D.

; APPLICANT: Kinney, Anthony J.

; TITLE OF INVENTION: Plant Sugar Transport Proteins

; FILE REFERENCE: BB1163USDIV

; CURRENT APPLICATION NUMBER: US/11/210,316

; CURRENT FILING DATE: 2005-08-24

; PRIOR APPLICATION NUMBER: US/10/051,902

; PRIOR FILING DATE: 2002-01-17

; PRIOR APPLICATION NUMBER: 60/083,044

; PRIOR FILING DATE: 1998-04-24



GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 13, 2006, 18:47:51 ; Search time 44 Seconds  
 (without alignments)  
 1622.565 Million cell updates/sec

Title: US-10-725-189-2  
 Perfect score: 3911  
 Sequence: 1 MEEGFRDRAAFIRGAKDIAK.....LALGSSLALKLPETRGQVLQ 742

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : PIR\_80:\*  
 1: pir1:\*  
 2: pir2:\*  
 3: pir3:\*  
 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3886	99.4	742	2	S27263	synaptic vesicle p
2	3879	99.2	742	1	A43344	synaptic vesicle p
3	2440	62.4	724	2	I50531	transmembrane tran
4	2337	59.8	683	2	S34961	synaptic vesicle p
5	488.5	12.5	454	2	F75580	probable sugar tra
6	465.5	11.9	448	2	AC3602	transporter, mfs s
7	464.5	11.9	437	2	G97630	probable sugar tra
8	464.5	11.9	437	2	AB2854	MFS permease [impo
9	442.5	11.3	450	2	F95360	probable transmemb
10	425	10.9	529	2	T23190	hypothetical prote
11	409	10.5	455	2	B83213	probable MFS trans
12	395.5	10.1	400	2	C69757	transporter homolo
13	371	9.5	461	2	AE3208	MFS permease [impo

14	334.5	8.6	452	2	G91007	probable transport
15	328	8.4	452	2	AI0779	probable n-hydroxy
16	327.5	8.4	452	2	A85852	probable transport
17	303	7.7	422	2	G72234	hypothetical prote
18	291.5	7.5	300	2	S15786	glucose transport
19	289.5	7.4	521	2	S67491	phosphate transpor
20	281.5	7.2	423	2	S74046	probable sugar tra
21	263	6.7	556	2	S50862	organic cation tra
22	261	6.7	452	2	AD0300	probable transport
23	260.5	6.7	446	2	B83033	probable MFS trans
24	260.5	6.7	461	2	D70073	metabolite transpo
25	259.5	6.6	448	2	B90498	permease, probable
26	258	6.6	557	2	JW0089	organic cation tra
27	257.5	6.6	449	2	AB2887	MFS permease [impo
28	257.5	6.6	477	2	G97662	benzoate transport
29	257	6.6	508	2	G84564	probable sugar tra
30	249.5	6.4	448	2	G83616	4-hydroxybenzoate
31	247.5	6.3	560	2	T51485	sugar transporter-
32	246.5	6.3	451	2	S66008	transport protein
33	244	6.2	442	2	A83122	probable MFS trans
34	235.5	6.0	407	2	C64167	hypothetical prote
35	235	6.0	471	2	H90502	phosphate transpor
36	235	6.0	568	2	T43734	phosphate transpor
37	235	6.0	592	2	S43742	hexose transport p
38	235	6.0	593	2	JC4884	organic cation tra
39	233.5	6.0	566	2	S51081	glucose transport
40	233	6.0	511	2	A84537	probable sugar tra
41	231.5	5.9	419	2	E69888	metabolite transpo
42	231	5.9	489	2	G90422	sugar transport pr
43	231	5.9	547	2	C84593	probable sugar tra
44	230	5.9	455	2	F97065	D-xylose-proton sy
45	229.5	5.9	567	2	S31294	hexose transport p

#### ALIGNMENTS

##### RESULT 1

S27263

synaptic vesicle protein SV2 - bovine

N;Alternate names: transporter-like protein p87

C;Species: Bos primigenius taurus (cattle)

C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004

C;Accession: S27263

R;Gingrich, J.A.; Andersen, P.H.; Tiberi, M.; El Mestikawy, S.; Jorgensen, P.N.; Freneau Jr., R.T.; Caron, M.G.

FEBS Lett. 312, 115-122, 1992

A;Title: Identification, characterization, and molecular cloning of a novel transporter-like protein localized to the central nervous system.

A;Reference number: S27263; MUID:93050176; PMID:1426240

A;Accession: S27263

A;Molecule type: mRNA

A;Residues: 1-742 <GIN>

A;Cross-references: UNIPROT:Q29397; UNIPARC:UPI0000088011; GB:S47919;

NID:g259173; PIDN:AAB24028.1; PID:g259174

C;Superfamily: synaptic vesicle protein SV2

OM protein - protein search, using sw model

Run on: February 13, 2006, 18:44:22 ; Search time 237 Seconds  
 (without alignments)  
 2208.869 Million cell updates/sec

Title: US-10-725-189-2  
 Perfect score: 3911  
 Sequence: 1 MEEGFRDRAAFIRGAKDIAK.....LALGSSLALKLPETRQVLQ 742

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : UniProt\_05.80:\*  
 1: uniprot\_sprot:\*  
 2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	3911	100.0	742	2	Q7L0J3_HUMAN	Q7l0j3 homo sapien
2	3911	100.0	748	2	O94841_HUMAN	O94841 homo sapien
3	3897	99.6	742	2	Q7Z3L6_HUMAN	Q7z3l6 homo sapien
4	3892	99.5	742	2	Q5R4L9_PONPY	Q5r4l9 pongo pygma
5	3890	99.5	742	2	Q4R4X3_MACFA	Q4r4x3 macaca fasc
6	3886	99.4	742	2	Q29397_BOVIN	Q29397 bos taurus
7	3883	99.3	742	2	Q9JIS5_MOUSE	Q9jis5 mus musculu
8	3879	99.2	742	2	Q58DZ8_RAT	Q58dz8 rattus norv
9	3868	98.9	742	1	SV2_RAT	Q02563 rattus norv
10	3810	97.4	748	2	Q80TT0_MOUSE	Q80tt0 mus musculu
11	3626	92.7	682	2	Q5QNX8_HUMAN	Q5qnx8 homo sapien
12	3595	91.9	682	2	Q8NBj6_HUMAN	Q8nbj6 homo sapien
13	3180	81.3	604	2	Q9BVZ9_HUMAN	Q9bvz9 homo sapien
14	2989.5	76.4	751	2	Q4SEK4_TETNG	Q4sek4 tetraodon n
15	2968	75.9	776	2	Q4SJ29_TETNG	Q4sj29 tetraodon n

16	2464.5	63.0	727	2	Q9Z2I6_RAT	Q9z2i6	rattus norv
17	2457.5	62.8	752	2	Q69ZS6_MOUSE	Q69zs6	mus musculu
18	2440	62.4	724	2	Q90406_DISOM	Q90406	discopyge o
19	2363	60.4	734	2	Q4RUQ4_TETNG	Q4ruq4	tetraodon n
20	2358	60.3	760	2	Q4S265_TETNG	Q4s265	tetraodon n
21	2352	60.1	683	2	Q8BG39_MOUSE	Q8bg39	m mus muscu
22	2337	59.8	683	2	Q63564_RAT	Q63564	rattus norv
23	2336.5	59.7	707	2	O94840_HUMAN	O94840	homo sapien
24	2325.5	59.5	683	2	Q6IAR8_HUMAN	Q6iar8	homo sapien
25	2325.5	59.5	683	2	Q7L1I2_HUMAN	Q7l1i2	homo sapien
26	2157	55.2	588	2	Q80TT1_MOUSE	Q80tt1	mus musculu
27	1972.5	50.4	797	2	Q4S8C4_TETNG	Q4s8c4	tetraodon n
28	1722	44.0	332	2	Q8R0R5_MOUSE	Q8r0r5	mus musculu
29	1633.5	41.8	480	2	Q9UPU8_HUMAN	Q9upu8	homo sapien
30	834.5	21.3	540	2	Q4SLU3_TETNG	Q4slu3	tetraodon n
31	688.5	17.6	632	2	Q9W3W9_DROME	Q9w3w9	drosophila
32	660	16.9	773	2	Q6U1H1_CTEFE	Q6ulh1	ctenocephal
33	645	16.5	596	2	Q7QGU8_ANOGA	Q7qgu8	anopheles g
34	638.5	16.3	513	2	Q5TVR1_ANOGA	Q5tvr1	anopheles g
35	573	14.7	287	2	Q4TDX6_TETNG	Q4tdx6	tetraodon n
36	515	13.2	156	2	Q8JZZ9_MOUSE	Q8jzz9	mus musculu
37	502.5	12.8	496	2	Q4HBE1_9DEIO	Q4hbe1	deinococcus
38	488.5	12.5	454	2	Q9RYN9_DEIRA	Q9ryn9	deinococcus
39	484.5	12.4	501	2	Q7QES5_ANOGA	Q7qes5	anopheles g
40	469	12.0	401	2	O61531_AEDAL	O61531	aedes albop
41	466.5	11.9	588	2	Q7XPE1_ORYSA	Q7xpe1	oryza sativ
42	465.5	11.9	436	2	Q577T5_BRUAB	Q577t5	brucella ab
43	465.5	11.9	448	2	Q8YBZ6_BRUME	Q8ybz6	brucella me
44	464.5	11.9	437	2	Q8UD68_AGR5	Q8ud68	agrobacteri
45	461.5	11.8	436	2	Q8FWC4_BRUSU	Q8fwc4	brucella su

#### ALIGNMENTS

##### RESULT 1

Q7L0J3\_HUMAN

ID Q7L0J3\_HUMAN PRELIMINARY; PRT; 742 AA.

AC Q7L0J3;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)

DE Synaptic vesicle glycoprotein 2 (Synaptic vesicle glycoprotein 2A).

GN Name=SV2A; ORFNames=RP11-196G18.19-001;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Ovary;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,